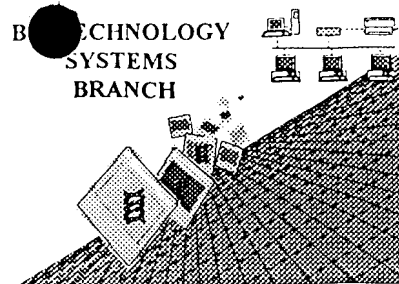


Romeo

BIOTECHNOLOGY
SYSTEMS
BRANCH



#13
DMT
3-9-01

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/267,963 A

Source: 1647

Date Processed by STIC: 3-9-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable-form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

1647

RAW SEQUENCE LISTING DATE: 03/09/2001
 PATENT APPLICATION: US/09/267,963A TIME: 10:53:19

Input Set : A:\- LUD-5539.1 SEQUENCE LISTING.asci.txt
 Output Set: N:\CRF3\03092001\I267963A.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
 5 (i) APPLICANT: Kohei MIYAZONO; Takeshe IMAMURA; Peter DEN DIJKE
 7 (ii) TITLE OF INVENTION: ISOLATED ALK-1 PROTEIN, NUCLEIC ACIDS ENCODING
 8 IT, AND USES THEREOF
 10 (iii) NUMBER OF SEQUENCES: 46
 12 (iv) CORRESPONDENCE ADDRESS:
 13 (A) ADDRESSEE: Fulbright & Jaworski L.L.P.
 14 (B) STREET: 666 Fifth Avenue
 15 (C) CITY: New York City
 16 (D) STATE: New York
 17 (E) COUNTRY: USA
 18 (F) ZIP: 10103
 20 (v) COMPUTER READABLE FORM:
 21 (A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
 22 (B) COMPUTER: IBM PS/2
 23 (C) OPERATING SYSTEM: PC-DOS
 24 (D) SOFTWARE: Wordperfect
 26 (vi) CURRENT APPLICATION DATA:
 C--> 27 (A) APPLICATION NUMBER: US/09/267,963A
 C--> 28 (B) FILING DATE: 12-Mar-1999
 29 (C) CLASSIFICATION: 435
 63 (vii) PRIOR APPLICATION DATA:
 32 (A) APPLICATION NUMBER: PCT/GB93/02367
 33 (B) FILING DATE: November 17, 1993
 36 (A) APPLICATION NUMBER: GB 9224057.1
 37 (B) FILING DATE: November 17, 1992
 40 (A) APPLICATION NUMBER: GB 9304677.9
 41 (B) FILING DATE: March 8, 1993
 44 (A) APPLICATION NUMBER: GB 9304680.3
 45 (B) FILING DATE: March 8, 1993
 48 (A) APPLICATION NUMBER: 9311047.6
 49 (B) FILING DATE: May 28, 1993
 52 (A) APPLICATION NUMBER: 9313763.6
 53 (B) FILING DATE: July 2, 1993
 56 (A) APPLICATION NUMBER: 9136099.2
 57 (B) FILING DATE: August 3, 1993
 60 (A) APPLICATION NUMBER: 321344.5
 61 (B) FILING DATE: October 15, 1993
 64 (A) APPLICATION NUMBER: 09/039,177
 65 (B) FILING DATE: March 13, 1998
 67 (viii) ATTORNEY/AGENT INFORMATION:
 68 (A) NAME: Mary Anne Schofield
 69 (B) REGISTRATION NUMBER: 36,669
 70 (C) REFERENCE/DOCKET NUMBER: LUD 5539.1 CIP - JEL/MAS
 72 (ix) TELECOMMUNICATION INFORMATION:
 73 (A) TELEPHONE: (212) 318-3000

Does Not Comply
 Corrected Diskette Needed
 See pp. 2, 4, 5, 6, 7

RAW SEQUENCE LISTING DATE: 03/09/2001
 PATENT APPLICATION: US/09/267,963A TIME: 10:53:19

Input Set : A:\- LUD-5539.1 SEQUENCE LISTING.asci.txt
 Output Set: N:\CRF3\03092001\I267963A.raw

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(B) TELEFAX: (212) 318-3400

ERRORED SEQUENCES

2641 (2) INFORMATION FOR SEQ ID NO: 32:
 2642 (i) SEQUENCE CHARACTERISTICS:
 2643 (A) LENGTH: 175 amino acids
 2644 (B) TYPE: amino acid
 2645 (D) TOPOLOGY: linear
 2647 (ii) MOLECULE TYPE: peptide
 2649 (vi) ORIGINAL SOURCE:
 2650 (A) ORGANISM: Mouse
 2652 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:
 2654 Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys Ala
 2655 5 10 15
 2656 Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln Asp
 2657 20 25 30
 2658 Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly Met
 2659 35 40 45
 2660 Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly Thr
 2661 50 55 60
 2662 Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys Gly
 2663 65 70 75 80
 2664 Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu Leu
 2665 85 90 95
 2666 Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His Glu
 2667 100 105 110
 2668 Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His Arg
 2669 115 120 125
 2670 Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala Cys
 2671 130 135 140
 2672 Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser Ala
 2673 145 150 155 160
 2674 Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro
 E--> 2675

*Misaligned amino
 acid numbering
 see # 4 on
 Error
 Summary
 Sheet.*

2797 (2) INFORMATION FOR SEQ ID NO: 35:
 2798 (i) SEQUENCE CHARACTERISTICS:
 2799 (A) LENGTH: 536 amino acids
 2800 (B) TYPE: amino acid
 2801 (D) TOPOLOGY: linear
 2803 (ii) MOLECULE TYPE: peptide
 2805 (vi) ORIGINAL SOURCE:
 2806 (A) ORGANISM: MOUSE
 2808 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:
 2810 Met Thr Ala Pro Trp Ala Ala Leu Ala Leu Leu Trp Gly Ser Leu Cys
 2811 5 10 15
 2812 Ala Gly Ser Gly Arg Gly Glu Ala Glu Thr Arg Glu Cys Ile Tyr Tyr
 2813 20 25 30

use "spaces" not "tabs"

RAW SEQUENCE LISTING

DATE: 03/09/2001

PATENT APPLICATION: US/09/267,963A

TIME: 10:53:20

Input Set : A:\- LUD-5539.1 SEQUENCE LISTING.asci.txt

Output Set: N:\CRF3\03092001\I267963A.raw

```

2814 Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser Gly Leu Glu Arg
2815          35          40          45
2816 Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr Ala Ser Trp Arg
2817          50          55          60
2818 Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Lys Gly Cys Trp Leu Asp
2819 65          70          75          80
2820 Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala Thr Glu Glu Asn
2821          85          90          95
2822 Pro Gln Val Tyr Phe Cys Cys Cys Glu Gly Asn Phe Cys Asn Glu Arg
2823          100          105          110
2824 Phe Thr His Leu Pro Glu Pro Gly Gly Pro Glu Val Thr Tyr Glu Pro
2825          115          120          125
2826 Pro Pro Thr Ala Pro Thr Leu Leu Thr Val Leu Ala Tyr Ser Leu Leu
2827          130          135          140
2828 Pro Ile Gly Gly Leu Ser Leu Ile Val Leu Leu Ala Phe Trp Met Tyr
2829 145          150          155          160
2830 Arg His Arg Lys Pro Pro Tyr Gly His Val Asp Ile His Glu Val Arg
2831          165          170          175
2832 Gln Cys Gln Arg Trp Ala Gly Arg Arg Asp Gly Cys Ala Asp Ser Phe
2833          180          185          190
2834 Lys Pro Leu Pro Phe Gln Asp Pro Gly Pro Pro Pro Pro Ser Pro Leu
2835          195          200          205
2836 Val Gly Leu Lys Pro Leu Gln Leu Leu Glu Ile Lys Ala Arg Gly Arg
2837          210          215          220
2838 Phe Gly Cys Val Trp Lys Ala Gln Leu Met Asn Asp Phe Val Ala Val
2839 225          230          235          240
2840 Lys Ile Phe Pro Leu Gln Asp Lys Gln Ser Trp Gln Ser Glu Arg Glu
2841          245          250          255
2842 Ile Phe Ser Thr Pro Gly Met Lys His Glu Asn Leu Leu Gln Phe Ile
2843          260          265          270
2844 Ala Ala Glu Lys Arg Gly Ser Asn Leu Glu Val Glu Leu Trp Leu Ile
2845          275          280          285
2846 Thr Ala Phe His Asp Lys Gly Ser Leu Thr Asp Tyr Leu Lys Gly Asn
2847          290          295          300
2848 Ile Ile Thr Trp Asn Glu Leu Cys His Val Ala Glu Thr Met Ser Arg
2849 305          310          315          320
2850 Gly Leu Ser Tyr Leu His Glu Asp Val Pro Trp Cys Arg Gly Glu Gly
2851          325          330          335
2852 His Lys Pro Ser Ile Ala His Arg Asp Phe Lys Ser Lys Asn Val Leu
2853          340          345          350
2854 Leu Lys Ser Asp Leu Thr Ala Val Leu Ala Asp Phe Gly Leu Ala Val
2855          355          360          365
2856 Arg Phe Glu Pro Gly Lys Pro Pro Gly Asp Thr His Gly Gln Val Gly
2857          370          375          380
2858 Thr Arg Arg Tyr Met Ala Pro Glu Val Leu Glu Gly Ala Ile Asn Phe
2859 385          390          395          400
2860 Gln Arg Asp Ala Phe Leu Arg Ile Asp Met Tyr Ala Met Gly Leu Val
2861          405          410          415
2862 Leu Trp Glu Leu Val Ser Arg Cys Lys Ala Ala Asp Gly Pro Val Asp

```

RAW SEQUENCE LISTING

DATE: 03/09/2001

PATENT APPLICATION: US/09/267,963A

TIME: 10:53:20

Input Set : A:\- LUD-5539.1 SEQUENCE LISTING.asci.txt

Output Set: N:\CRF3\03092001\I267963A.raw

2863 420 425 430
 2864 Glu Tyr Met Leu Pro Phe Glu Glu Glu Ile Gly Gln His Pro Ser Leu
 2865 435 440 445
 2866 Glu Glu Leu Gln Glu Val Val Val His Lys Lys Met Arg Pro Thr Ile
 2867 450 455 460
 2868 Lys Asp His Trp Leu Lys His Pro Gly Leu Ala Gln Leu Cys Val Thr
 2869 465 470 475 480
 2870 Ile Glu Glu Cys Trp Asp His Asp Ala Glu Ala Arg Leu Ser Ala Gly
 2871 485 490 495
 2872 Cys Val Glu Glu Arg Val Ser Leu Ile Arg Arg Ser Val Asn Gly Thr
 2873 500 505 510
 2874 Thr Ser Asp Cys Leu Val Ser Leu Val Thr Ser Val Thr Asn Val Asp
 E--> 2875 515 520 525
 2876 Leu Leu Pro Lys Glu Ser Ser Ile
 E--> 2877 530 535
 3069 (2) INFORMATION FOR SEQ ID NO: 38:
 3070 (i) SEQUENCE CHARACTERISTICS:
 3071 (A) LENGTH: 6 amino acids
 3072 (B) TYPE: amino acid
 3073 (D) TOPOLOGY: linear
 3075 (ii) MOLECULE TYPE: peptide
 3077 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:
 3079 Asp Leu Lys Pro Glu Asn
 E--> 3080 5
 3083 (2) INFORMATION FOR SEQ ID NO: 39:
 3084 (i) SEQUENCE CHARACTERISTICS:
 3085 (A) LENGTH: 6 amino acids
 3086 (B) TYPE: amino acid
 3087 (D) TOPOLOGY: linear
 3089 (ii) MOLECULE TYPE: peptide
 3091 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:
 3093 Asp Leu Ala Ala Arg Asn
 E--> 3094 5
 3096 (2) INFORMATION FOR SEQ ID NO: 40:
 3097 (i) SEQUENCE CHARACTERISTICS:
 3098 (A) LENGTH: 6 amino acids
 3099 (B) TYPE: amino acid
 3100 (D) TOPOLOGY: linear
 3102 (ii) MOLECULE TYPE: peptide
 3104 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:
 3106 Asp Ile Lys Ser Lys Asn
 E--> 3107 5
 3110 (2) INFORMATION FOR SEQ ID NO: 41:
 3111 (i) SEQUENCE CHARACTERISTICS:
 3112 (A) LENGTH: 6 amino acids
 3113 (B) TYPE: amino acid
 3114 (D) TOPOLOGY: linear
 3116 (ii) MOLECULE TYPE: peptide
 3118 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

*Misaligned amino
acid numbering.*

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/267,963A

DATE: 03/09/2001
 TIME: 10:53:20

Input Set : A:\- LUD-5539.1 SEQUENCE LISTING.asci.txt
 Output Set: N:\CRF3\03092001\I267963A.raw

```

3120 Asp Phe Lys Ser Lys Asn
E--> 3121      ← 5
3124 (2) INFORMATION FOR SEQ ID NO: 42:
3125     (i) SEQUENCE CHARACTERISTICS:
3126         (A) LENGTH: 6 amino acids
3127         (B) TYPE: amino acid
3128         (D) TOPOLOGY: linear
3130     (ii) MOLECULE TYPE: peptide
3132     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:
3134 Asp Leu Lys Ser Ser Asn
E--> 3135      ← 5
3138 (2) INFORMATION FOR SEQ ID NO: 43:
3139     (i) SEQUENCE CHARACTERISTICS:
3140         (A) LENGTH: 6 amino acids
3141         (B) TYPE: amino acid
3142         (D) TOPOLOGY: linear
3144     (ii) MOLECULE TYPE: peptide
3146     (ix) FEATURE:
3147         (D) OTHER INFORMATION: First Xaa is Thr or Ser;
3148 fourth Xaa is Tyr or Phe; Each other Xaa
3149 may be any amino acid
3151     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:
W--> 3153 Gly Xaa Xaa Xaa Xaa Xaa
E--> 3154      ← 5
3157 (2) INFORMATION FOR SEQ ID NO: 44:
3158     (i) SEQUENCE CHARACTERISTICS:
3159         (A) LENGTH: 6 amino acids
3160         (B) TYPE: amino acid
3161         (D) TOPOLOGY: linear
3163     (ii) MOLECULE TYPE: peptide
3165     (ix) FEATURE:
3166         (D) OTHER INFORMATION: First Xaa is any amino acid;
3167 second Xaa is Ile or Val;
3168 third Xaa is Lys or Arg;
3169 fourth Xaa is Thr or Met.
3171     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:
W--> 3173 Xaa Pro Xaa Xaa Trp Xaa
E--> 3174      ← 5
3177 (2) INFORMATION FOR SEQ ID NO: 45:
3178     (i) SEQUENCE CHARACTERISTICS:
3179         (A) LENGTH: 6 amino acids
3180         (B) TYPE: amino acid
3181         (D) TOPOLOGY: linear
3183     (ii) MOLECULE TYPE: peptide
3185     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:
3187 Gly Thr Arg Arg Tyr Met
E--> 3188      ← 5
3190 (2) INFORMATION FOR SEQ ID NO: 46:
3191     (i) SEQUENCE CHARACTERISTICS:

```

*Misaligned amino
acid numbering*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/267,963A

DATE: 03/09/2001

TIME: 10:53:20

Input Set : A:\- LUD-5539.1 SEQUENCE LISTING.asci.txt

Output Set: N:\CRF3\03092001\I267963A.raw

3192 (A) LENGTH: amino acids
3193 (B) TYPE: amino acid
3194 (D) TOPOLOGY: linear
3196 (ii) MOLECULE TYPE: peptide
3198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:
3200 Gly Thr Ala Arg Tyr Met
E--> 3201 5 ↗

→ No length given for
Sequence #46.

09/267, 963

p. 7

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1984 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

→ should be header # IV
This error occurs elsewhere
in the sequence listing.
Please check and correct

09/267, 9631

p. 8

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 513 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

Type

VERIFICATION SUMMARY

DATE: 03/09/2001

PATENT APPLICATION: US/09/267,963A

TIME: 10:53:21

Input Set : A:\- LUD-5539.1 SEQUENCE LISTING.asci.txt

Output Set: N:\CRF3\03092001\I267963A.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:88 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:333 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:604 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:889 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1144 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1398 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1640 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1897 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2149 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2392 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2410 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2428 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2446 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2464 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2482 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2500 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2519 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:2675 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:32
L:0 M:200 E: Mandatory Header Field missing, Seq 34, [(B) TYPE:] of (2)(i)
L:2875 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
M:332 Repeated in SeqNo=35
L:0 M:200 E: Mandatory Header Field missing, Seq 37, [(B) TYPE:] of (2)(i)
L:3080 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:38
L:3094 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:39
L:3107 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:40
L:3121 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:41
L:3135 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:42
L:3153 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:3154 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:43
L:3173 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:3174 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:44
L:3188 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:45
L:3201 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:46
L:3201 M:203 E: No. of Seq. differs, LENGTH:Input:0 Found:6 SEQ:46